



SEQUENCE LISTING

<110> De Buyl, Eric
Lahaye, Andree
Ledoux, Pierre
Detroz, Rene

<120> Xylanase, Microorganisms Producing it,
DNA Molecules, Methods for Preparing this Xylanase and Uses
of the Latter

<130> GC450-D1-US

<140> US 09/909,207
<141> 2001-07-19

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<151> 1995-06-06

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aacaaatgtta acaacatatt attccgtaaa ggtaaaaat tcaatgaaac acaaacacac 180
caacaagttg gtaacatgtc cataaactac ggagccaact tccaacccaa tggtaatgcg 240
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tggggcaact ggcgtccacc aggagcaacg cctaaggga ccatcactgt tgatggagga 360
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tttaaacaat attggagtgt tcgaagatcg aaacgcacga gtggcacat ttctgtcagc 480
aaccacttta gagcgtggga aaacttaggg atgaatatgg gggaaatgtta tgaagtgcg 540
cttactgttag aaggctatca aagtagcggaa agtgcataatg tatatacgaa tacactaaga 600
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20 25 30

ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc 144
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe
35 40 45

cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa gtt ggt 192
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
50 55 60

aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg 240
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
65 70 75 80

tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat 288
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
85 90 95

att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag 336
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100 105 110

ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt 384
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
115 120 125

aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat 432
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130 135 140

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145 150 155 160

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165 170 175

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Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
180 185 190

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 35 40 45
 Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
 50 55 60
 Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
 65 70 75 80
 Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
 85 90 95
 Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
 100 105 110
 Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
 115 120 125
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 130 135 140
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 145 150 155 160
 Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
 165 170 175
 Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
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 195 200 205
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 tatgattatg aattttggaa agatagcggt ggctctggga caatgattct caatcatggc 180
 ggtacgttca gtgcccattt gaaacatgtt aacaacatat tattccgtaa agttaaaaaaa 240
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 ttccaaccaa atggtaatgc gtatttatgc gtctatggtt ggactgttga ccctcttgc 360
 gaatattata ttgtcgacag ttggggcaac tggcgccac caggagcaac gcctaagggg 420
 accatcactg ttgatggagg aacatatgtt atctacgaga ctcttagagt caatcaaccc 480
 tccattaagg ggattgccac attaaacaa tattggagtg ttcgaagatc gaaacgcacg 540
 agtggcacga tttctgtcag caaccactt agagcgtggg aaaacttagg gatgaatatg 600
 gggaaaatgt atgaagtcgc gcttactgta gaaggctatc aaagttagcg aagtgctaat 660

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 Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
 20 25 30
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 aat tcc att ggc aac cac gat ggc tat gat tat gaa ttt tgg aaa gat 144
 Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
 35 40 45
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 agc ggt ggc tct ggg aca atg att ctc aat cat ggc ggt acg ttc agt 192
 Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
 50 55 60
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 gcc caa tgg aac aat gtt aac aac ata tta ttc cgt aaa ggt aaa aaa 240
 Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
 65 70 75 80
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 Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
 85 90 95
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 100 105 110
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 Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
 115 120 125
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 Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
 130 135 140
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 Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro

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tcc att aag ggg att gcc aca ttt aaa caa tat tgg agt gtt cga aga				528
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg				
165	170	175		
tcg aaa cgc acg agt ggc acg att tct gtc agc aac cac ttt aga gcg				576
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala				
180	185	190		
tgg gaa aac tta ggg atg aat atg ggg aaa atg tat gaa gtc gcg ctt				624
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu				
195	200	205		
act gta gaa ggc tat caa agt agc gga agt gct aat gta tat agc aat				672
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn				
210	215	220		
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Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu				
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35	40	45		
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser				
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Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys				
65	70	75	80	
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn				
85	90	95		
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr				
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Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp				
115	120	125		
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val				
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Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro				
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<213> *Bacillus* sp.

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Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala
 1 5 10

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Phe Leu Val Cys Phe Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala				
caa atc gtc acc gac aat tcc att ggc aac cac gat ggc tat gat tat	30	35	40	748
Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr				
gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat	45	50	55	796
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His				
ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc	60	65	70	844
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe				
cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt	80	85	90	892
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly				
aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg	95	100	105	940
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala				
tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat	110	115	120	988
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr				
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Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys				
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Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu				
aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat	160	165	170	1132
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr				
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Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser				
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Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala				
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Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr				
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Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
240 245

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ataggaactt tcccatttgc aagacgataa aaaatcttt tcccctattt tatcttATCG 180
ccttgcattgg tttaatttgt aaactttattt ttagttacg tgatgttccc tcattcatac 240
cattaatcac agttaacgct agagtcatct ttttcgggtt ctcaaaaata cctgaagaac 300
atttatgtca tattttctca cgccgctcca taatggata tatatactct tttatacata 360
ttaagtaaat tagtatac ttgcgttattc aaaatgtgag ataatcta atgtcaaaca 420
agcagctatc caaaaaacac tgatgttgc ac tcttaaaga agtgcacta tctatgaaaa 480
gataattatc cagtttcaaa atttgaataa gtgttatgg aatagtttga atgtcaactg 540
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gaggaatgct tgaaacacct ccgtcactag 150

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<213> Artificial Sequence

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<220>
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